

PhD placement/PIPS: Transposable Elements in ash-tree resistance to ash dieback

Placement supervisor:

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Placement department:

Trait Diversity and Function

Placement overview and objectives:

Natural tree populations are exposed to increasing threats posed by biotic and abiotic stressors. One recent case with large predicted ecological and economic consequences is ash dieback disease, currently decimating ash (*Fraxinus excelsior*) populations in the UK and northern Europe.

Although there is evidence that ash populations are adapting to the disease via selection on standing genetic variation, it is still unclear if this process will be fast enough to conserve populations. In addition, most studies focused on identifying genetic resistance to the disease have only investigated Single Nucleotide Polymorphisms.

Transposable Elements (TEs) and other Structural Variants (SVs) have the potential to quickly generate large amounts of *de-novo* genetic variation, and their activity can be triggered by stressful conditions, making them a potential source of resistance that has been under-investigated thus far.

This placement aims to investigate TE composition in a newly assembled *F. excelsior* genome and variation in a large collection of trees of this species, collected in forests in the south of England. It is part of a larger NERC funded project focusing on the role of SVs in ash adaptation to the ash dieback epidemic and will have access to a large Whole Genome Sequencing dataset generated within this project.

Tasks to be undertaken/possible projects:

- Improving the current TE annotation for the newly generated *F. excelsior* reference genome, including the identification of transposons and their classification.
- Detecting transposon insertions or absences in natural populations compared to the reference genome using short-read whole genome sequencing.
- Depending on interest, other molecular phenotypes such as genome or telomere size can be investigated in ash natural populations. These aspects of genome structure and stability can also potentially be affected by stress and could constitute responses to ash dieback disease.

Required skills and experience:

- An interest in genetics, conservation and evolutionary biology
- Some basic understanding of the Linux environment and command line usage will be necessary to navigate the compute cluster where the data are stored and to proceed with the analyses.

Skills and areas of knowledge that can be developed:

- Collaborating in an ambitious research-oriented project and work with colleagues in the Plant Health and Adaptation team.
- Navigating a High-Performance Cluster and running software for DNA sequencing data analysis.
- Learning TE annotation in a high-quality reference genome.
- Understanding of TE biology and their dynamics in natural populations.

Location of work:

Kew Gardens (Jodrell building) with the possibility of hybrid work and working from home after discussion

Length of placement:

3 months or longer